

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/579,693
Source: IFWP
Date Processed by STIC: 5/31/06

ENTERED



IFWP

RAW SEQUENCE LISTING

DATE: 05/31/2006

PATENT APPLICATION: US/10/579,693

TIME: 13:29:04

Input Set : E:\seqlist.txt

Output Set: N:\CRF4\05312006\J579693.raw

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4 <110> APPLICANT: BASF AKTIENGESELLSCHAFT et al.
6 <120> TITLE OF INVENTION: METHODS FOR THE PREPARATION OF A FINE
7   CHEMICAL BY FERMENTATION
10 <130> FILE REFERENCE: BGI-159PC2
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/579,693
C--> 13 <141> CURRENT FILING DATE: 2006-05-18
15 <150> PRIOR APPLICATION NUMBER: PCT/IB2003/006464
16 <151> PRIOR FILING DATE: 2003-12-18
18 <160> NUMBER OF SEQ ID NOS: 15
20 <170> SOFTWARE: FastSEQ for Windows Version 4.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 1650
24 <212> TYPE: DNA
25 <213> ORGANISM: Corynebacterium glutamicum
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (101)...(1627)
31 <400> SEQUENCE: 1
32 accaacgacg acgccggtgt agcagatgta ttggagtggt ggttctaata ggtggtgta 60
33 aaacactgct tagtggccca atacgtgcaa aaataaggcc atg aga atc tca aag 115
34                                     Met Arg Ile Ser Lys
35                                     1       5
37 gcc aat gcg tat gtt gca gcg att gac caa ggc acc act tcc act cgg 163
38 Ala Asn Ala Tyr Val Ala Ala Ile Asp Gln Gly Thr Thr Ser Thr Arg
39             10             15             20
41 tgc atc ttc att gat gcc caa gga aaa gtg gtg tct tct gct tcc aag 211
42 Cys Ile Phe Ile Asp Ala Gln Gly Lys Val Val Ser Ser Ala Ser Lys
43             25             30             35
45 gag cac cgc caa atc ttc cca caa cag ggc tgg gta gag cac gat cct 259
46 Glu His Arg Gln Ile Phe Pro Gln Gln Gly Trp Val Glu His Asp Pro
47             40             45             50
49 gaa gaa att tgg gac aac att cga tct gtc gtc agc cag gcg atg gtc 307
50 Glu Glu Ile Trp Asp Asn Ile Arg Ser Val Val Ser Gln Ala Met Val
51             55             60             65
53 tcc att gac atc acc cca cac gag gtt gca tcg ctg gga gtc acc aac 355
54 Ser Ile Asp Ile Thr Pro His Glu Val Ala Ser Leu Gly Val Thr Asn
55             70             75             80             85
57 cag cgc gaa acc acc gtg gtg tgg gac aag cac acc ggc gaa cct gtc 403
58 Gln Arg Glu Thr Val Val Trp Asp Lys His Thr Gly Glu Pro Val
59             90             95             100
61 tac aac gca atc gtg tgg caa gac acc cgc acc tct gac att tgc cta 451
62 Tyr Asn Ala Ile Val Trp Gln Asp Thr Arg Thr Ser Asp Ile Cys Leu
63             105             110             115

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65 gag atc gcg ggc gaa gaa ggc cag gaa aag tgg ctt gac cgc acc ggc 499
66 Glu Ile Ala Gly Glu Glu Gly Gln Glu Lys Trp Leu Asp Arg Thr Gly
67      120      125      130
69 ctg ctg atc aac tcc tac cca tcg ggg ccc aaa atc aag tgg att ctc 547
70 Leu Leu Ile Asn Ser Tyr Pro Ser Gly Pro Lys Ile Lys Trp Ile Leu
71      135      140      145
73 gac aac cct gag gga gct cgc gaa cgc gcc gaa aag ggc gac ctt ttg 595
74 Asp Asn Val Glu Gly Ala Arg Glu Arg Ala Glu Lys Gly Asp Leu Leu
75 150      155      160      165
77 ttt ggc acc atg gat acc tgg gtg ctg tgg aac ctg acc ggc ggt gtc 643
78 Phe Gly Thr Met Asp Thr Trp Val Leu Trp Asn Leu Thr Gly Gly Val
79      170      175      180
81 cgc ggc gac gac ggt gat gat gcc atc cac gtc acc gat gtc acc aac 691
82 Arg Gly Asp Asp Gly Asp Asp Ala Ile His Val Thr Asp Val Thr Asn
83      185      190      195
85 gca tcc cgc aca cta ttg atg gat ctc cgc acg caa cag tgg gat cca 739
86 Ala Ser Arg Thr Leu Leu Met Asp Leu Arg Thr Gln Gln Trp Asp Pro
87      200      205      210
89 gaa cta tgc gaa gcc cta gac att ccg atg tcc atg etc cct gag atc 787
90 Glu Leu Cys Glu Ala Leu Asp Ile Pro Met Ser Met Leu Pro Glu Ile
91      215      220      225
93 cgt ccc tcc gtc gga gaa ttc cgc tcc gtg cgc cac cgc gga acc cta 835
94 Arg Pro Ser Val Gly Glu Phe Arg Ser Val Arg His Arg Gly Thr Leu
95 230      235      240      245
97 gcc gac gtc ccg att act ggc gtg ctc ggc gac cag caa gcg gcc ctt 883
98 Ala Asp Val Pro Ile Thr Gly Val Leu Gly Asp Gln Gln Ala Ala Leu
99      250      255      260
101 ttt ggt cag ggc gga ttc cac gaa ggt gct gct aaa aat acc tac ggc 931
102 Phe Gly Gln Gly Gly Phe His Glu Gly Ala Ala Lys Asn Thr Tyr Gly
103      265      270      275
105 acc ggc ctc ttc ctg ctg atg aac acc ggc acc tcg ttg aag att tcc 979
106 Thr Gly Leu Phe Leu Leu Met Asn Thr Gly Thr Ser Leu Lys Ile Ser
107      280      285      290
109 gag cac ggc ctg ctg tcc acc atc gcc tat caa cgg gaa gga tcc gct 1027
110 Glu His Gly Leu Leu Ser Thr Ile Ala Tyr Gln Arg Glu Gly Ser Ala
111      295      300      305
113 ccg gtc tac gcg ctg gaa ggt tcc gta tcc atg ggc ggt tcc ttg gtg 1075
114 Pro Val Tyr Ala Leu Glu Gly Ser Val Ser Met Gly Gly Ser Leu Val
115 310      315      320      325
117 cag tgg ctg cgc gac aac cta cag cta atc ccc aac gca cca gcg att 1123
118 Gln Trp Leu Arg Asp Asn Leu Gln Leu Ile Pro Asn Ala Pro Ala Ile
119      330      335      340
121 gaa aac ctc gcc cga gaa gtc gaa gac aac ggt ggc gtt cat gtt gtc 1171
122 Glu Asn Leu Ala Arg Glu Val Glu Asp Asn Gly Gly Val His Val Val
123      345      350      355
125 cca gca ttc acc gga ctg ttc gca cca cgt tgg cgc ccc gat gct cgt 1219
126 Pro Ala Phe Thr Gly Leu Phe Ala Pro Arg Trp Arg Pro Asp Ala Arg
127      360      365      370
129 ggc gtc att aca ggc ctc acc cgt ttt gcc aac cgc aaa cac atc gcc 1267

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130 Gly Val Ile Thr Gly Leu Thr Arg Phe Ala Asn Arg Lys His Ile Ala
131      375                      380                      385
133 cgc gca gtc ctt gaa gcc aac gcc ttc caa acc cgc gaa gtt gtg gac 1315
134 Arg Ala Val Leu Glu Ala Asn Ala Phe Gln Thr Arg Glu Val Val Asp
135 390                      395                      400                      405
137 gcc atg gcc aaa gac gca ggc aaa gcc ctc gaa tcc ctc cgc gtc gac 1363
138 Ala Met Ala Lys Asp Ala Gly Lys Ala Leu Glu Ser Leu Arg Val Asp
139                      410                      415                      420
141 ggt gcg atg gtg gaa aat gac ctc ctc atg caa atg caa gcc gac ttc 1411
142 Gly Ala Met Val Glu Asn Asp Leu Leu Met Gln Met Gln Ala Asp Phe
143                      425                      430                      435
145 ctc ggc atc gac gtc caa cgt ctc gag gac gta gaa acc acc gcc gtc 1459
146 Leu Gly Ile Asp Val Gln Arg Leu Glu Asp Val Glu Thr Thr Ala Val
147                      440                      445                      450
149 ggc gtc gca ttc gct gca ggt ctc ggc tct gga ttc ttc aaa aca act 1507
150 Gly Val Ala Phe Ala Ala Gly Leu Gly Ser Gly Phe Phe Lys Thr Thr
151                      455                      460                      465
153 gac gag atc gaa aaa ctt att gca gtg aag aaa gtc tgg aac cct gac 1555
154 Asp Glu Ile Glu Lys Leu Ile Ala Val Lys Lys Val Trp Asn Pro Asp
155 470                      475                      480                      485
157 atg agc gaa gaa gag cgc gaa cgt cgc tat gcc gaa tgg aat agg gca 1603
158 Met Ser Glu Glu Glu Arg Glu Arg Arg Tyr Ala Glu Trp Asn Arg Ala
159                      490                      495                      500
161 gtg gag cat tct tat gac cag gcc tagctgattt gggtcggcct tta 1650
162 Val Glu His Ser Tyr Asp Gln Ala
163                      505
166 <210> SEQ ID NO: 2
167 <211> LENGTH: 509
168 <212> TYPE: PRT
169 <213> ORGANISM: Corynebacterium glutamicum
171 <400> SEQUENCE: 2
172 Met Arg Ile Ser Lys Ala Asn Ala Tyr Val Ala Ala Ile Asp Gln Gly
173 1      5      10      15
174 Thr Thr Ser Thr Arg Cys Ile Phe Ile Asp Ala Gln Gly Lys Val Val
175      20      25      30
176 Ser Ser Ala Ser Lys Glu His Arg Gln Ile Phe Pro Gln Gln Gly Trp
177      35      40      45
178 Val Glu His Asp Pro Glu Glu Ile Trp Asp Asn Ile Arg Ser Val Val
179      50      55      60
180 Ser Gln Ala Met Val Ser Ile Asp Ile Thr Pro His Glu Val Ala Ser
181 65      70      75      80
182 Leu Gly Val Thr Asn Gln Arg Glu Thr Thr Val Val Trp Asp Lys His
183      85      90      95
184 Thr Gly Glu Pro Val Tyr Asn Ala Ile Val Trp Gln Asp Thr Arg Thr
185      100     105     110
186 Ser Asp Ile Cys Leu Glu Ile Ala Gly Glu Glu Gly Gln Glu Lys Trp
187      115     120     125
188 Leu Asp Arg Thr Gly Leu Leu Ile Asn Ser Tyr Pro Ser Gly Pro Lys
189      130     135     140

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190 Ile Lys Trp Ile Leu Asp Asn Val Glu Gly Ala Arg Glu Arg Ala Glu
191 145 150 155 160
192 Lys Gly Asp Leu Leu Phe Gly Thr Met Asp Thr Trp Val Leu Trp Asn
193 165 170 175
194 Leu Thr Gly Gly Val Arg Gly Asp Asp Gly Asp Asp Ala Ile His Val
195 180 185 190
196 Thr Asp Val Thr Asn Ala Ser Arg Thr Leu Leu Met Asp Leu Arg Thr
197 195 200 205
198 Gln Gln Trp Asp Pro Glu Leu Cys Glu Ala Leu Asp Ile Pro Met Ser
199 210 215 220
200 Met Leu Pro Glu Ile Arg Pro Ser Val Gly Glu Phe Arg Ser Val Arg
201 225 230 235 240
202 His Arg Gly Thr Leu Ala Asp Val Pro Ile Thr Gly Val Leu Gly Asp
203 245 250 255
204 Gln Gln Ala Ala Leu Phe Gly Gln Gly Phe His Glu Gly Ala Ala
205 260 265 270
206 Lys Asn Thr Tyr Gly Thr Gly Leu Phe Leu Leu Met Asn Thr Gly Thr
207 275 280 285
208 Ser Lys Lys Ile Ser Glu His Gly Leu Leu Ser Thr Ile Ala Trp Gln
209 290 295 300
210 Arg Glu Gly Ser Ala Pro Val Tyr Ala Leu Glu Gly Ser Val Ser Met
211 305 310 315 320
212 Gly Gly Ser Leu Val Gln Trp Leu Arg Asp Asn Leu Gln Leu Ile Pro
213 325 330 335
214 Asn Ala Pro Ala Ile Glu Asn Leu Ala Arg Glu Val Glu Asp Asn Gly
215 340 345 350
216 Gly Val His Val Val Pro Ala Phe Thr Gly Leu Phe Ala Pro Arg Trp
217 355 360 365
218 Arg Pro Asp Ala Arg Gly Val Ile Thr Gly Leu Thr Arg Phe Ala Asn
219 370 375 380
220 Arg Lys His Ile Ala Arg Ala Val Leu Glu Ala Asn Ala Phe Gln Thr
221 385 390 395 400
222 Arg Glu Val Val Asp Ala Met Ala Lys Asp Ala Gly Lys Ala Leu Glu
223 405 410 415
224 Ser Leu Arg Val Asp Gly Ala Met Val Glu Asn Asp Leu Leu Met Gln
225 420 425 430
226 Met Gln Ala Asp Phe Leu Gly Ile Asp Val Gln Arg Leu Glu Asp Val
227 435 440 445
228 Glu Thr Thr Ala Val Gly Val Ala Phe Ala Ala Gly Leu Gly Ser Gly
229 450 455 460
230 Phe Phe Lys Thr Thr Asp Glu Ile Glu Lys Leu Ile Ala Val Lys Lys
231 465 470 475 480
232 Val Trp Asn Pro Asp Met Ser Glu Glu Glu Arg Glu Arg Arg Tyr Ala
233 485 490 495
234 Glu Trp Asn Arg Ala Val Glu His Ser Tyr Asp Gln Ala
235 500 505
238 <210> SEQ ID NO: 3
239 <211> LENGTH: 35
240 <212> TYPE: DNA

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Input Set : E:\seqlist.txt

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241 <213> ORGANISM: Artificial Sequence
243 <220> FEATURE:
244 <223> OTHER INFORMATION: Oligonucleotide
246 <400> SEQUENCE: 3
247 gagagagaga cgcgtcccgag tggctgagac gcac 35
249 <210> SEQ ID NO: 4
250 <211> LENGTH: 34
251 <212> TYPE: DNA
252 <213> ORGANISM: Artificial Sequence
254 <220> FEATURE:
255 <223> OTHER INFORMATION: Oligonucleotide
257 <400> SEQUENCE: 4
258 ctctctctgt cgacgaattc aatcttacgg cctg 34
260 <210> SEQ ID NO: 5
261 <211> LENGTH: 4323
262 <212> TYPE: DNA
263 <213> ORGANISM: Corynebacterium glutamicum
265 <400> SEQUENCE: 5
266 tagagaggac tgacgtcggg ccggtcagca cgcgtcatat gactagtctg gacctaggga 60
267 tatcgtcgac atcgatgctc ttctgcgtta attaacaatt gggatcctct agaccgaggga 120
268 tttaaatcgc tagcgggctg ctaaagggaag cggaacacgt agaaagccag tccgcagaaa 180
269 cgggtgctgac ccgggatgaa tgtcagctac tgggctatct ggacaaggga aaacgcaagc 240
270 gcáaagagaa agcaggtagc ttgcagtggg cttacatggc gatagctaga ctgggcgggtt 300
271 ttatggacag caagcgaacc ggaattgcca gctggggcgc cctctggtaa gggtgggaag 360
272 ccctgcaaag taaactggat ggctttcttg ccgccaaagg tctgatggcg caggggatca 420
273 agatctgatc aagagacagg atgaggatcg ttctgcatga ttgaacaaga tggattgcac 480
274 gcaggttctc cggccgcttg ggtggagagg ctattcggct atgactgggc acaacagaca 540
275 atcggctgct ctgatgccgc cgtgttccgg ctgtcagcgc aggggcgccc gggtcttttt 600
276 gtcaagaccg acctgtccgg tgccctgaat gaactgcagg acgaggcagc gcggctatcg 660
277 tggctggcca cgacgggcgt tccttgccga gctgtgctcg acgttgtcac tgaagcggga 720
278 agggactggc tgctattggg cgaagtgccg gggcaggatc tcctgtcatc tcaccttgct 780
279 cctgccgaga aagtatccat catggctgat gcaatgcggc ggctgcatac gcttgatccg 840
280 gctacctgcc cattcgacca ccaagcgaaa catcgcatcg agcagcacag tactcggatg 900
281 gaagccggtc ttgtcgatca ggatgatctg gacgaagagc atcaggggct cgcgccagcc 960
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283 ggcatgacct gcttgccgaa tatcatggtg gaaaatggcc gcttttcttg attcatcgac 1080
284 tgtggccggc tgggtgtggc ggaccgctat caggacatag cgttggctac ccgtgatatt 1140
285 gctgaagagc ttggcggcga atgggctgac cgcttcctcg tgctttacgg tatcgccgct 1200
286 cccgattcgc agcgcacgcg cttctatcgc cttcttgacg agttcttctg agcgggactc 1260
287 tgggggttca aatgaccgac caagcgacgc ccaacctgcc atcacgagat ttcgattcca 1320
288 ccgccgcctt ctatgaaagg ttgggcttcg gaatcgtttt ccgggacgcc ggctggatga 1380
289 tcctccagcg cggggatctc atgctggagt tcttcgcccc cgctagcggc gcgccggccg 1440
290 gcccgtgtg aaataccgca cagatgcgta aggagaaaat accgcatcag gcgctcttcc 1500
291 gcttctcgc tcactgactc gctgcgctcg gtcgttcggc tgcggcgagc ggtatcagct 1560
292 cactcaaaag cgtaataacg gttatccaca gaatcagggg ataacgcagg aaagaacatg 1620
293 tgagcaaaaag gccagcaaaa ggccaggaac cgtaaaaagg ccgctgtgct ggcgtttttc 1680
294 cataggctcc gccccctga cgagcatcac aaaaatcgac gctcaagtca gaggtggcga 1740
295 aaccgacag gactataaag ataccaggcg tttccccctg gaagctccct cgtgcgctct 1800
296 cctgttccga ccctgccgct taccggatac ctgtccgcct ttctcccttc ggaagcgtg 1860

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/579,693

DATE: 05/31/2006

TIME: 13:29:05

Input Set : E:\seqlist.txt

Output Set: N:\CRF4\05312006\J579693.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application Number

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date